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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Sat May 13 09:58:28 2000; MasPar time 4.62 Seconds 230.882 Million cell updates/sec

Title:

Description:
Perfect Score:
Sequence: >US-09-331-631-3
(29-73) from US09331631.pep (2 of 5)
361
1 SEFDRQEYEECKROCMQLETSGOMRRCVSQCDKRFEEDIDWSKYD 45

Scoring table: PAM 150 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35 1:geneseqp

Statistics: Mean 24.753; Variance 88.190; scale 0.281

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

22 23	154 177	1111 10087654321	Result
72 72 71 71	77 73 73	361 361 259 109 97 95 95	Score
19.9	- 22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	100.0 100.0 71.7 30.2 26.9 26.3 26.3 26.3 21.3	% Query Match
1416 2703 2710	444 489 524 81 125 125	5555 5555 5555 5555 5555 5555 5555 5555 5555	Length
44444		, , 44444444 ,	DB
W62835 R67358 R70236 W22482	W90341 W90341 W90339 Y12435 R13329 W81779	W62829 W62829 W62830 W62830 W62831 W62831 W62831 W62831 W40281 W40282 W40283 W40342 W40342 W40342	IJ.
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/note= "signal peptide"

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ω	Human slit 3 mature pr	Thermostable T. aquati	A thermophilic ligase	Thermus aquaticus DNA	Homo sapiens B223 sequ	P. aeruginosa mucA.	Cyclic corticotrophin	(Cyclo 30-33)[D-Phe12,	Human transient recept	Mycobacterium species	ILTV thymidine kinase.	Mycobacterium species	Human type C lectin.	WD-40 domain-contg. Mu	Arabidopsis enhanced d	Antimicrobial maize pe	Zea mays antimicrobial	Neisseria polyglycosyl	N. gonorrhoeae glycosy	Human 5' EST secreted	Plasmodium var-7.
1.29e+02	1.29e+02	1.29e+02	1.29e+02	1.29e+02	1.29e+02	1.29e+02	1.29e+02	1.29e+02	1.06e+02	1.06e+02	1.06e+02	1.06e+02	8.70e+01	8.70e+01	8.70e+01	7.13e+01	7.13e+01	5.83e+01	5.83e+01	5.83e+01	4.77e+01

## ALIGNMENTS

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tide	Macadamia integrifolia. Kev	bial protein; infestation; c	27-OCT-1998 (first entry) Macadamia integrifolia antimicrobial protein.	LT 2 W62828 standard; Protein; 666 AA.	29 SEFDRQEYEECKRQCMQLETSGQMRRCVSQCDKRFEEDIDWSKYD 73	29 SEFDRQEYEECKROCMQLETSGOMRRCVSQCDKRFEEDIDWSKYD 73	45; Conservative	Query Match 100.0%; Score 361; DB 1; Length 666; Best Local Similarity 100.0%; Pred. No. 2.58e-30;	Sequence 666 AA;	imals.	The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammalian	Claim 1; Page 39-41; 96pp; English.	useful for controlling microbial infestations of plants or mammals	Novel anti-microbial protein from e.g. Macadamia integrifolia		KC, Green JL, Mann		20-DRC-1996: AU-004275			/note=	96	Peptide 128		•	antimicrobial protein; infestation; control.	1998 (first entry)		W62829 standard: Protein: 666 AA.	

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22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL
Bower NI, Goulter KC, Green JI
WPI; 98-377279/32.
                     W62832 standard; Protein; 590 AA.
W62832;
27-CCT-1998 (first entry)
Gossypium hirsutum antimicrobial protein.
Gossypium birsutum; infestation; control.
Gossypium hirsutum.
W09827805-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for controlling microbial infestations of plants or mammal: Claim 1; Page 43-45; 96pp; English.

The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammalian
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The sequence is that of an antimicrobial protein which
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Similarity 100.0%;
32; Conservative
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Similarity 100.0%;
45; Conservative
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Green JL, Manners JM, Marcus JP;
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Pred. No. 9.96e-19;
0; Mismatches (
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1. No. 2.58e-30;
Mismatches 0
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Matches 1
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07-JUN-1991; G00914.
11-JUN-1990; GB-013016.
(MRSC) MARS UK LTD.
Spencer ME, Hodge R, Deakin E
WPI; 92-024418/03.
N-PSDB; Q20377.
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Novel anti-microbial protein from e.g. Macadamia integruseful for controlling microbial infestations of plants claim 1; Page 47-49; 96pp; English.

The sequence is that of an antimicrobial protein which microbial infestations in plants and
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22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
Bower NI, Goulter KC, Green JL, Manners JM, May
MPI; 98-377279/32.
                    expression vectors
Claim 4; Fig 2; 59
                                                                                                                                                                                                                                                                  Theobroma cacao. WO9119801-A.
                                                                                                                                                                                                                                                                                                           Cocoa; flavour; vicilin; seed storage protein.
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The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and man
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Sequence encoded by 67 kD T. cacao protein cDNA
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20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
  Claim 4; Fig 2; 59pp; English
The inventors claim a 67 kD a
                                                                  beans and produced
                                                                                    Recombinant cocoa proteins - are
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larity 45.2%;
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Pred. No. 1.26e-02;
6; Mismatches 10
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bial infestations
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1.88e-01;
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  cacao
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yeast and ba
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16-JUL-1997, 112154.
16-JUL-1996; US-680845.
(MIXS/) MIXSON A J.
MIXSON AJ.
                                                                            R40823 stand
R40823;
R40823;
03-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragments, and encoding DNAs. The 47 kD and 31 kD proteins are derived from the 67 kD precursor. T. cacao protein CDNA was detected in a cDNA library prepared from immature cocoa beans RNA using a probe based on the AA sequence of a CNBr peptide common to the 47 kD and 31 kD polypeptides. Homology searches revealed close homologies between the 67 kD polypeptide and the vicilins, which are seed storage proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the thrombospondin gene TSP1 which is used in a method to produce a cationic vehicle consisting of a cationic liposome: DNA complex where the DNA encodes an anti-angiogenic peptide or tumour suppressor protein. Such complexes are used for treatment of neopleastic and metabolic diseases especially for gene therapy of tumours.
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W40287
Human thrombospondin 1. hTSP-1; platelet glycoprotein; inhibitor; solid tumour; skin c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human TSP1 protein.

TSP1; thrombospondin; anti-angiogenic; cationic vehicle; gene therapy;
liposome; DNA complex; tumour suppressor protein; treatment; neoplastic;
metabolic disease; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 98-078839/08.
N-PSDB; V10493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complexes of DNA encoding anti-angiogenic peptide - with cationic liposome(s) or cationic polymer, useful for, e.g. gene therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP-819758-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-AUG-1998
                                                                                                                                                                                                                                                                               116 SSVOTRTCHIQECDKRFKQDGGWS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laim
                                                                                                                                                                                                                                     48
                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity les 11; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Page 6; 47pp; English.
                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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llarity 31.4%;
Conservative
                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "encoded by CGG" 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
199. .2:
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                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                            26.3%;
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Pred. No. 1.88e-01;
11; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                         Score 95; DB 1; I
Pred. No. 2.93e-01;
                                                                                                                                                                                                                                                                                                                                 4;
; angiogenesis; neovascularisation;
cancer; angiogenic dysfunction;
                                                                                                                                                                                                                                     70
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Matches 12; Consei
                                                                                                                                                                                                                 21-JAN-1998.
16-JUL-1997; 112154.
16-JUL-1996; US-680845.
(MIXS/) MIXSON A J.
MIXSON AJ;
                                                            This protein sequence represents a concatamer of thrombospondin Ts which is used in a method to produce a cationic vehicle consisting of a cationic liposome:DNA complex where the DNA encodes an anti-anglogenic peptide or tumour suppressor protein. Such complex used for treatment of neoplastic and metabolic diseases especially gene therapy of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human concatamerised TSPI protein.
TSPI; thrombospondin; anti-angiogenic; cationic vehicle; gene therapy; liposome; DNA complex; tumour suppressor protein; treatment; neoplastimetabolic disease; concatamer; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W40288 standard; Protein; W40288; 18-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Certain fragments of thrombospondin, a glycoprotein found in alpha granules of platelets, can inhibit vascularisation. Per derived from the hTSP sequence are useful for inhibiting neovascularisation, esp. in solid tumours such as melanomas. Inhibitory peptides can also be used in other diseases involvangiogenic dysfunction. See R40824-R40830.
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Bouck NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-SEP-1993.
22-FEB-1993: U01652.
24-FEB-1992: US-841656.
(NOUN) UNIV NORTHWESTERN!
                                                                                                                                                               Complexes of DNA encoding anti-angiogenic peptide - with cationic liposome(s) or cationic polymer, useful for, e.g. gene therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compsn. for inhibiting angiogenesis inhibitor comprising a peptide capal
                                                Sequence
                                                                                                                                      Claim 9; Page 6-7; 47pp; English.
                                                                                                                                                                                           N-PSDB; V10494
                                                                                                                                                                                                                                                                                   EP-819758-A2.
                                                                                                                                                                                                                                                                                                                                    Misc_difference
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WO9316716-A.
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Kaposi's sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vascularisation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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sarcoma; inflammation;
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larity 50.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                              /note=
221
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383
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            26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
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                                                                                                                                                                                                                                                                                               intervening sequence
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Score
Pred.
4; M
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Pred. No. 2.93e-01;
4; Mismatches 7;
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            No. 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polverini
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    contg. a vascu
ble of inhibiting

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         DB 1; Lo
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                                                                                        Such complexes
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Peptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T New isolated plant Id gene - used to develop prods. for use i altering the induction of flowering in plants

S Claim 7; Fig 3 and Fig 5; 58pp; English.

C The Id gene controls flower evocation in maize plants. The maize nucleic acid is similar to that of genes encoding zinc-

C finger regulatory proteins in animals.

C Transposons Ac and Ds constitute a family of related transpos celements present in maize. A derivative of Ds, Ds2, can be u to produce a new mutant of the Id gene. The Ds2 (in the present in the present constitute and inserted into the Id gene to produce id*.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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                New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds Claim 7; Page 39-40; SBpp; English.

This sequence represents a novel sucrose binding protein, SBP2 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to produce a n of active Ac) and inserted i Sequence 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G. max truncated SBP2 protein.
SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maize;
Ds2; f
                                                                                                                                                                                                                                                                                                                                                                                   Chao WS, Grimes HD; WPI; 99-070155/06.
                                                                                                                                                                                                                                                                                                                                                                                                                  26-NOV-1998.
21-MAY-1998; U10465.
21-MAY-1997; US-047568.
22-MAY-1997; US-047568.
(UNIV WASHINGTON STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine max
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31-OCT-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9853086-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seed; carbohydrate content; soybean.
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N-PSDB; T42174, T42175.
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16-MAR-1995; US-406186.
(COLD-) COLD SPRING HARBOR LAB
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Zea mays; Id; id*; transposon; transposable element;
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Similarity 35.0%;
7; Conservative
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No.
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increase the carbohydrate
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                                                                                                                                                                                                          DE G. max runcated SBP1 protein.

W SBP1; sucrose binding protein; SBP2; s
Glycine max.

WO9853086-A1.
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Best Local S
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Best Local
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18-FEB-1998; U03161.
30-DEC-1997; US-000640.
20-FEB-1997; US-804104.
(COLD-) COLD SPRING HARBOR LACCOLASANTI JJ, Sundaresan V;
WPI, 98-407564/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express anv Sequence 409 AA.
Chao WS, Grimes HD;
WPI; 99-070155/06.
New modified plant sucrose binding proteins -
transgenic plants which can have enhanced or d
uptake activity in developing seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               id gene controlling floral induction in maize - useful to create transgenic plants with earlier, delayed or inhibited floral induction e.g. to extend geographical range of crops Claim 5; Fig 3; 68pp; English.

The maize Id gene controls floral induction and is useful in the production of transgenic plants with altered floral induction times, i.e. earlier, delayed or inhibited floral induction. The Id gene and zinc-ringer regulatory regions are useful to identify these genes in maize and isolate similar genes in other plants. The polypeptides and antibodies are also useful in Id detection e.g. to locate activity
                                                                                                                                       21-MAY-1998; U10465.
22-MAY-1997; US-047568.
(UNIW) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays.
W09837201-A1.
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Similarity 45.8%;
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larity 35.0%;
Conservative
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                                                                                                                                            STATE RES
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Pred. No. 1.39e+01;
6; Mismatches 7
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6; M
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No.
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. 1.39e+01;
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PI Chao WS, Grimes HD;

DR WFI; 99-070155/06.

PI New modified plant sucrose binding proteins - used to develop

PI transgenic plants which can have enhanced or decreased sucrose

PI uptake activity in developing seeds

CC laim 13D; Page 37-38; 58pp; English.

PS Claim 13D; Page 37-38; 58pp; English.

CC production of a modified plant sucrose binding protein, SBP2 isolated

CC from Glycine max. This protein is used in a method resulting in the

CC production of a modified plant sucrose binding protein (SBP) which has a

CC modified amino acid sequence compared to a corresponding wild-type SBP,

CC and where expression of the modified SBP in a yeast assay system confers

CC mhanced sucrose uptake compared to the corresponding transgenic plants

CC which have modified sucrose uptake activity in developing transgenic plants

CC seeds. Enhanced sucrose uptake activity in developing seeds may be

CC desirable where it is an advantage to increase the carbohydrate content

CC seeds might be desirable where the seed is the primary plant material harvested,

CC such as soybean). In contrast, decreased sucrose uptake activity in

CC such as sybbean). In contrast, decreased sucrose uptake activity in

CC such as sybbean). In contrast, decreased sucrose uptake activity in

CC such as sybbean and so may be used to express any

CC such as Apa Apa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches 1
                                                                                                                               Matches
                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 36-37; 58pp; English.

This sequence represents a novel sucrose binding protein, SBP1 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. The products of the invention can be used for producing transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant; seed; carbohydrate content; soybean.
                                                                                                                                                                                                                                                                 Sequence
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22-MAY-1997; US-047568.
(UNIW ) UNIV WASHINGTON STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAY-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity nes 11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity nes 12; Conser
39
                            42 CKHQCQQQRQYTESDKRTCLQQCD 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     max SBP2 protei
                                                                                                                                                                                                                                                              489 AA;
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                                                                                                                           Conservative
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                                                                                                                                                           21.3%;
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                                                                                                                    Score 77; DB 1; 1
Pred. No. 1.39e+01
6; Mismatches 1
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Pred. No. 1.39e+01;
6; Mismatches 6
60
                                                                                                                                                                                           Length 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 444;
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RESULT

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The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be consistent of the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in seed in the plant is seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any
                                                                                                                                                             Query Match
Best Local S
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucross uptake activity in developing seeds Disclosure; Page 34-36; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-MAY-1997; US-047568.
(UNIW ) UNIV WASHINGTON STATE RES FOUND. Chao WS, Grimes HD; WPI; 99-770155/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G. max SBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-NOV-1998; U10465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seed; carbohydrate content; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                    transgene in
                                              43 CKHQCQQQQQYTEGDKRVCLQSCD-RY 68
39 CKRQCMQLE--TSGQMRRCVSQCDKRF
                                                                                                                                                    21.3%;
Similarity 44.4%;
12; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               max
                                                                                                                                                                                                                                                                                                                              in developing seeds. 524 AA;
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                                                                                                                                                        Score 77; DB 1; 1
Pred. No. 1.39e+01,
6; Mismatches (
    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or decreased sucrose
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